177. (New) A hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8 or the sequence perfectly complementary thereto.

* * * * *

Remarks

Claims 39-42, 48-51, 54-56, 67-73, 75, 78-80, 82-84, 86, 88-90, 92, 93 and 95-177 are presently pending in the subject application.

Reconsideration and allowance in view of the above amendments, the following remarks and the attached Declarations Under 37 C.F.R. § 1.131 are respectfully requested.

The specification has been amended herein to correct clerical mistakes in the data provided in Example 5. These clerical mistakes do not alter Applicants' showing that a blocked promoter-primer can be combined with a primer to amplify a target nucleic acid sequence and are evident from the Declaration data of co-inventor Yeasing Yang provided herewith. (The Declaration data of Yeasing Yang is the basis for example 5.) Applicants wish to point out that data for test samples including a cordycepin blocked promoter-primer, an alkane diol blocked promoter-primer and an unblocked promoter-primer in the Declaration data of Yeasing Yang was not included in the results of Example 5 because a selection reagent was accidentally added to these test samples.

The claims have been amended herein to place them in better form for consideration on appeal.

Claims 76, 77, 85, 87 and 91 have been canceled herein without prejudice to the prosecution of the subject matter of these claims in this or a future continuing application.

In a review of internal documents, it was determined that oligonucleotides comprising the nucleotide base sequence of SEQ ID NO: 2, and its complement, were previously discovered by

employees of Gen-Probe Incorporated who are not co-inventors of the subject application. Accordingly, claim 39 has been amended herein to specify that the claimed kit includes the pair of recited oligonucleotides, and claim 40 has been amended herein to eliminate reference to a nucleic acid sequence of SEQ ID NO: 2 or a fully complementary sequence of the same length. All claims now pending which recite an oligonucleotide comprising or targeting the nucleotide base sequence of SEQ ID NO: 2 or its complement are claimed in combination with at least one fully patentable oligonucleotide. Thus, these claimed combinations are likewise fully patentable.

Claims 39-41 have been amended herein to indicate that the nucleotide base sequence of the first recited sequence corresponds to SEQ ID NO: 22. If "x" is a sequence recognized by an RNA polymerase, then the nucleotide base sequence may correspond to SEQ ID NO: 1.

Claim 40 has been further amended herein to indicate that the claimed oligonucleotide is at least 22 bases in length. This limitation is consistent with the length of SEQ ID NO: 22.

Claims 40, 67, 69, 70, 96, 98, 143, 147, 151 and 152 have been amended herein to replace "fully complementary sequence of the same length thereof" with "sequence perfectly complementary thereto" for consistency in the claim language. Applicants submit that the two phrases are synonymous.

Claim 41 has been further amended herein to recite first and second oligonucleotides and to correct sequence errors in the claims. The corrected sequences are supported by the specification. Corrections to the sequences also necessitated adjusting the length limitation of the second oligonucleotide recited to at least 22 bases.

Claim 49 has been amended herein to recite a third oligonucleotide. This amendment comports with the language of amended claim 41, which recites first and second oligonucleotides.

Claim 54 has been amended herein to specifically recite a third oligonucleotide having a 3' end modified to reduce or block extension by a polymerase, where the modifications to the 3' ends of the second and third oligonucleotides are different. This language is supported by the original language of the claim and merely makes explicit what was previously implicit.

Claim 56 has also been amended herein to specifically recite a third oligonucleotide. In claim 56, however, the third oligonucleotide does not have a 3' end which has been modified to reduce or block extension by a polymerase. This language is supported by the original language of the claim and merely makes explicit what was previously implicit.

Claim 67, 75, 84, 101, 147, 158, 160, 162, 164 and 166 have been amended herein to indicate that the recited primer oligonucleotide will hybridize to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions. A number of non-limiting amplification procedures are described in the specification, (*see, e.g.*, specification at pages 3-6), which are well-known in the art. Those skilled in the art will readily appreciate various reaction conditions permitting a targeted nucleic acid sequence to be amplified using the claimed primer oligonucleotides. Moreover, the Examples section of the specification provides detailed amplification reaction conditions for using the claimed primer oligonucleotides in a transcription-mediated amplification procedure.

Claims 71, 78, 88 and 153 have been amended herein to functionally indicate that the further included nucleotide base sequence is recognized by an RNA polymerase which initiates transcription. This amendment is supported by the specification at, for example, the paragraph bridging pages 7 and 8. Applicants submit that this is a non-limiting clarification of the original claim language.

Claims 75 and 84 have been amended herein to recite compositions for amplification comprising first and second primer oligonucleotides. The language describing the claimed primer oligonucleotides has not been amended herein in a narrowing manner.

Claim 78 has been amended herein to depend from claim 75 only, as claims 76 and 77 have been canceled without prejudice herein.

Claims 79, 89, 96, 98, 101, 160, 164 and 167 have been amended herein to replace the phrase "nucleic acid hybridization assay probe" with the phrase "hybridization probe," consistent with Applicants' usage in the specification. *See, e.g.*, specification at page 29, line 29. Claims 79, 89, 96, 98, 101, 160, 164 and 167 have also been amended herein to indicate that the claimed probes

will hybridize with specificity to the recited region of *Mycobacterium tuberculosis* nucleic acid, or the complement thereof. The specification provides that an oligonucleotide which binds with specificity will be able to distinguish between target sequences and non-target sequences in the test environment. *See, e.g.*, specification at page 13, lines 4-7.

Claims 86 and 88 have been amended herein to reflect that the composition of claim 84 includes two primer oligonucleotides. In addition, claim 88 has been amended to depend from claim 84 or 86, as claim 85 has been canceled without prejudice herein.

Claims 96-99, 157, 161, 165, 168 and 169 have been amended herein to replace the phrase "helper probe" with the synonymous phrase "helper oligonucleotide." This amendment to the claims is supported in the specification at, for example, page 16, lines 3-15.

Claims 101, 160 and 164 have been amended herein to recite compositions useful in the detection of *Mycobacterium tuberculosis* comprising a hybridization probe and a primer oligonucleotide. These amendments are supported by the former language of claims 101, 160 and 164.

Claims 102 and 120 have been amended herein to indicate the claimed compositions do not require the presence of a target nucleic acid sequence. This amendment is consistent with the language of corresponding kit claims 139 and 141.

Claims 131 and 132 have been amended herein to depend from claim 129, consistent with the recitation of second and third primer sequences in these claims.

Claim 145 has been amended herein to clarify the claim language. The amendments to claim 145 are non-limiting.

Claim 146 has been amended herein to recite a third oligonucleotide. This amendment is consistent with the language of claim 145, which indicates that only one of the two claimed oligonucleotides includes a 3' end modification to reduce or block extension by a polymerase.

Claim 150 has been amended herein to indicate that the primer oligonucleotide of claim 69 is at least 22 nucleotide bases in length. This limitation is consistent with the length of SEQ ID NO: 22.

Claim 156 has been amended herein to clarify the claim language. The amendments to claim 156 are non-limiting.

Claim 158 has been converted into an independent claim herein, incorporating certain limitations of claim 101, from which it previously depended. The recited Markush grouping does not include primer oligonucleotides having the nucleotide base sequence of SEQ ID NO: 2. Otherwise, claim 158 has not been further limited.

Claim 159 has been converted into an independent claim herein, incorporating certain limitations of claim 101, from which it previously depended. The amendments to claim 159 are non-limiting.

Claims 159, 163 and 167 have been amended herein to emphasize that the targeted region of *Mycobacterium tuberculosis* which forms a detectable nucleic acid hybrid with the recited hybridization probe may be the RNA equivalent of the recited target region. This amendment is supported in the specification *passim* and in particular in Examples 1 and 2.

Claim 162 has been converted into an independent claim herein, incorporating certain limitations of claim 160, from which it previously depended. Excluded from amended claim 162 is a primer oligonucleotide having the nucleotide base sequence of SEQ ID NO: 1 or SEQ ID NO: 2. Otherwise, claim 162 has not been further limited.

Claim 163 has been converted into an independent claim herein, incorporating certain limitations of claim 160, from which it previously depended. The amendments to claim 163 are non-limiting.

Claim 166 has been converted into an independent claim herein, incorporating certain limitations of claim 164, from which it previously depended. Excluded from amended claim 166 is primer oligonucleotide having the nucleotide base sequence of SEQ ID NO: 6. Otherwise, claim 166 has not been further limited.

Claim 167 has been converted into an independent claim herein, incorporating certain limitations of claim 164, from which it previously depended. The amendments to claim 167 are non-limiting.

Claim 172 has been amended herein to clarify the claim language. The amendments to claim 172 are non-limiting.

The claims have also been amended herein to correct clerical and grammatical errors, to ensure proper antecedent basis, and to maintain uniformity of claim language throughout.

Claims 173-177 are newly added. The number of claims being added herein is equal to the number of claims being canceled.

New claim 173 depends from claim 162 and recites a second primer oligonucleotide, where the nucleotide base sequence of the target region of the second primer is the nucleotide base sequence of SEQ ID NO: 2 or the sequence perfectly complementary thereto. Support for this claim can be found in, for example, the language of claims 39 and 160.

New claim 174 depends from claim 166 and recites that the nucleotide base sequence of the target region is the nucleotide base sequence of SEQ ID NO: 23 or the sequence perfectly complementary thereto. Support for new claim 174 can be found in claim 166.

New claim 175 depends from claim 166 and recites that the nucleotide base sequence of the target region is the nucleotide base sequence of SEQ ID NO: 7 or the sequence perfectly complementary thereto. Support for new claim 175 can be found in claim 166.

New claim 176 is an independent claim which recites a hybridization probe, where the nucleotide base sequence region targeted by the probe is the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto. Support for new claim 176 can be found in claim 160 prior to amendment herein.

New claim 177 is an independent claim which recites a hybridization probe, where the nucleotide base sequence target region of the probe is the nucleotide base sequence of SEQ ID NO: 8 or the sequence perfectly complementary thereto. Support for new claim 177 can be found in claim 164 prior to amendment herein.

No new matter is believed to have been introduced by any of amendments to the claims herein.

Rejection Under 35 U.S.C. § 102

Claims 39, 40, 67, 69, 71-73, 75, 76, 78-80, 84-86, 88-91, 95-99, 101-104, 106-122, 124-143, 147-151, 156-162 and 164-167 stand rejected by the Examiner under 35 U.S.C. § 102(e) as being anticipated by Kacian *et al.* (U.S. Patent No. 5,554,516). In maintaining this rejection, the Examiner observes that SEQ ID Nos. 1, 3-6 and 8-10 of the instant application are identical to SEQ ID Nos. 14-17 and 10-13 of Kacian, respectively. Applicants submit that a first Declaration Under 37 C.F.R. § 1.131 submitted herewith, and signed by each of the co-inventors, overcomes this rejection by establishing that the inventors of the instant application conceived of and reduced to practice oligonucleotides consisting of the sequences of SEQ ID Nos. 1, 3-6 and 8-10 in the United States prior to May 6, 1992, the effective filing date of Kacian.

Exhibits A-H of the first Declaration constitute eight sequence request forms which were prepared by Diane McAllister for synthesizing oligonucleotides represented by SEQ ID Nos. 1, 3-6 and 8-10 of the instant application prior to May 6, 1992. Diane McAllister diligently submitted these sequence request forms to Liz Bescher, Mehrdad Majlessi and Sheryl Roberts for synthesis of the eight oligonucleotides corresponding to SEQ ID Nos. 1, 3-6 and 8-10. Using these sequence request forms as a template, Liz Bescher, Mehrdad Majlessi and Sheryl Roberts then diligently synthesized the requested oligonucleotides on DNA synthesizers prior to May 6, 1992 and recorded their activities in the laboratory notebook pages of Exhibits I-P. As these laboratory notebook pages evidence, the synthesized oligonucleotides were purified and their presence was confirmed by optical density measurements taken before and after the crude samples were purified.

For the reasons presented above, Applicants submit that Kacian has been properly sworn back of and is unavailable as a prior art reference for maintaining the Examiner's rejection.

Rejections Under 35 U.S.C. § 103

Claims 39-42, 48-51, 54-56, 67-69, 71-73, 75, 76, 78-80, 84-86, 88-93, 95-99, 101-104, 106-122 and 124-169 stand rejected by the Examiner under 35 U.S.C. § 103(a) as being unpatentable over Kacian (U.S. Patent No. 5,554,516). In maintaining this rejection, the Examiner cites Kacian for *inter alia* suggesting the following: (i) a composition comprising the sequences of instant SEQ ID Nos. 9 and 10; (ii) modifying Kacian's promoter-primer of SEQ ID NO: 14 to include a 3'-end modification which inhibits or prohibits extension reactions in that direction; (iii) instant SEQ ID NO: 3 is identical to Kacian's SEQ ID NO: 15; and (iv) kits and mixtures of promoter-primers including both modified and unmodified 3'-ends. Applicants respectfully traverse this rejection for the reasons that follow.

To the extent that the Examiner's rejection relies upon Kacian's disclosure of any of SEQ ID Nos. 10-17 (corresponding to instant SEQ ID Nos. 6, 8-10, 1 and 3-5, respectively), Applicants submit that this rejection has been overcome by the first Declaration Under 37 C.F.R. § 1.131 submitted herewith and described above in response to the Examiner' rejection under 35 U.S.C. § 102(e).

In response to the Examiner's contention that Kacian suggests mixtures of promoter-primers having both modified and unmodified 3' ends, Applicants are submitting herewith a second Declaration Under 37 C.F.R. § 1.131 establishing that the inventors of the instant application conceived of and reduced to practice compositions containing a primer and promoter-primers having both modified and unmodified 3' ends in the United States prior to May 6, 1992, the effective filing date of Kacian. This Declaration has been signed by each of the co-inventors.

Exhibit A of this second Declaration is taken from a laboratory notebook which was issued to Yeasing Yang. In this notebook, Yeasing Yang recorded the preparation of a test mixture containing 0.1 pmol unblocked promoter-primer and 15 pmol blocked promoter-primer, where the

blocked promoter-primer was modified to include cordycepin at its 3' end, prior to May 6, 1992. *See* Book No. 46 at page 46. The sequences of both promoter-primers were the same and are identified by the names"T7AMtbA-246-cordycepin" and "T7AMtbA-246," respectively. Also included in the mixture was 2 pmol primer, identified as "MgoA+146," 5 fg rRNA target from *Mycobacterium tuberculosis*, reverse transcriptase and T7 RNA polymerase. A control was also set up which was identical to the test mixture, except that no rRNA target was included.

Yeasing Yang then diligently proceeded to perform a transcription-based amplification procedure for each of the test and control samples prior to May 6, 1992, and the results of these amplifications were measured in relative light units (RLU). *See* Book No. 46 at page 47. RLU values for the test mixture correspond to test sample numbers 15-19 in the recorded results, and RLU values for the control correspond to test sample numbers 29 and 30 in the recorded results. The average RLU value for the control represents background signal. Subtracting background signal from the results corresponding to test sample numbers 15-19 clearly evidences that the rRNA target was amplified in the presence of the primer and the blocked and unblocked promoter-primers.

For the reasons presented above, Applicants submit that Kacian has been properly sworn back of and is unavailable as a prior art reference for maintaining the Examiner's rejection.

Change of Inventorship

In the course of identifying supporting documentation for the Declarations being filed herewith, Applicants' representative discovered that Yeasing Y. Yang had made an inventive contribution to certain claims of the subject application. Accordingly, Applicants are submitting herewith a Request to Correct Inventorship to include Yeasing Yang as a co-inventor of the subject application, as well as a new Declaration and Power of Attorney executed by all of the named inventors. As the Request being filed herewith indicates, the error in inventorship was inadvertent and occurred without deceptive intent on the part of Yeasing Yang.

Conclusion

Applicants submit that the subject application is in condition for allowance and Notice to the effect is respectfully requested.

Please charge any fees due in connection with this Amendment to Deposit Account No. 07-0835 in the name of Gen-Probe Incorporated.

Certificate of Transmission

I hereby certify that this correspondence (and any referred to as attached) is being sent by facsimile to 703-872-9307 on the date indicated below to Box AF, Commissioner for Patents, Washington, D.C. 20231.

Respectfully submitted,

Dated: April 3, 2002 By: _____

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Marked-Up Version of Amendments

IN THE SPECIFICATION:

The specification has been amended at page 29, lines 4-20, as follows:

Example 5

In this experiment, the effect of mixing a single oligonucleotide sequence with two different 3' modifications was demonstrated. Three tmol of target RNA was amplified as in Example 1. The promoter-primer was synthesized with an unblocked 3'-end, blocked with RP, or CO blocked. Two pmol of primer were used.

Pmol Promoter-primer			RLU
RP modified	CO modified	Unmodifed	
0	15	0.1	450,157
2	13	0 [0.01]	678,871 [681,647]
5 [2]	10 [13]	0.01 [0]	681,647 [678,871]
5	10	0	755,839

This example shows that a mixture of unmodified and modified or a mixture of different types of modified promoter-primers amplified well, allowing detection of 3 tmol of RNA target in one hour.

IN THE CLAIMS:

The claims have been amended as follows:

39. (Four Times Amended) A kit for amplifying *Mycobacterial* nucleic acid, said kit containing: [at least one of]

a first [and second] oligonucleotide[; said first oligonucleotide] comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT ([SEQ ID: 1 or 22] SEQ ID NO: 22)[,]; and

[said] a second oligonucleotide comprising the nucleotide base sequence of xGGGATAAGCCTGGGAAACTGGGTCTAATACC ([SEQ ID: 2] SEQ ID NO: 2),

wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein each said oligonucleotide is [about] from 22 to about 100 bases in length.

40. (Four Times Amended) An oligonucleotide of from [about 20] 22 to about 100 bases in length and comprising [a] the nucleotide base [nucleic acid] sequence [selected from the group consisting] of xGCCGTCACCCCACCAACAAGCT ([SEQ ID: 1 or 22] SEQ ID NO: 1 or SEQ ID NO: 22), [xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID: 2), and their] [fully complementary sequences of the same length] or the sequence perfectly complementary thereto, wherein x is nothing or is a sequence recognized by an RNA polymerase.

41. (Five Times Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide of from [about] 24 to about 100 bases in length and comprising [a] the nucleotide base sequence of GTCTTGTGGTGGAAAGCGCTTTAG ([SEQ ID: 3] SEQ ID NO: 3); and

[one or more of second oligonucleotides] a second oligonucleotide of from [about 23] 22 to about 100 bases in length and comprising a nucleotide base sequence selected from the group consisting of [xGCCGGTCACCCCACCAACAAGCT] xGCCGTCACCCCACCAACAAGCT ([SEQ ID: 1 or 22] SEQ ID NO: 22) and [xGGATAAGCCTGGGAAACTGGGTCTAATACC] xGGGATAAGCCTGGGAAACTGGGTCTAATACC ([SEQ ID: 2] SEQ ID NO: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase.

42. (Five Times Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide of from [about] 23 to about 100 bases in length and comprising [a] the nucleotide base sequence of [GGAGGATATGTCTCAGCGCTACC (SEQ ID: 8] SEQ ID NO: 8); and

[one or more of second oligonucleotides] a second oligonucleotide of from [about] 20 to about 100 bases in length and comprising a nucleotide base sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC ([SEQ ID: 6 or 23] SEQ ID NO: 23) and xCGCGGAACAGGCTAAACCGCACGC ([SEQ ID: 7] SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

48. (Three Times Amended) The kit of claim 41, wherein [one or more of] said second [oligonucleotides] oligonucleotide has a 3' end which is modified [at 3' end] to reduce or block extension of said [one or more of said] second [oligonucleotides] oligonucleotide by a polymerase.

49. (Three Times Amended) The kit of claim 48[, wherein one or more of said second oligonucleotides] further comprising a third oligonucleotide having a 3' end which is unmodified [at 3' end], wherein said third oligonucleotide is from 20 to about 100 bases in length and comprises a nucleotide base sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) and xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein the nucleotide base sequences of said second and third oligonucleotides are different.

50. (Three Times Amended) [An] The oligonucleotide of claim 40, wherein said oligonucleotide has a 3' end which is modified [at its 3' end] to reduce or block extension of said oligonucleotide by a polymerase.

51. (Four Times Amended) A composition comprising: [two or more oligonucleotides of claim 40, wherein one or more of said oligonucleotides is unmodified at the 3' end and one or more of said oligonucleotides]

a first oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said first oligonucleotide has a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said second oligonucleotide has a 3' end which is modified [at the 3' end] to reduce or block extension of said second oligonucleotide by a polymerase.

54. (Four Times Amended) The composition of claim 51 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension by a polymerase, wherein [one or more of] the 3' ends of said second and third oligonucleotides [is] are differently modified [at the 3' end to reduce or block extension by a polymerase].

55. (Three Times Amended) The kit of claim 42, wherein [one or more of] said second [oligonucleotides] oligonucleotide has a 3' end which is modified [at 3' end] to reduce or block extension of [said one or more of] said second [oligonucleotides] oligonucleotide by a polymerase.

56. (Three Times Amended) The kit of claim 55[, wherein one or more of said second oligonucleotides is unmodified at 3' end] further comprising a third oligonucleotide having a 3' end which is not modified to reduce or block extension of said third oligonucleotide by a polymerase.

67. (Three Times Amended) A primer oligonucleotide of from 10 to 100 nucleotide bases in length [able to hybridize] which hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid[,] under amplification reaction conditions, wherein the nucleotide base sequence of said region [consists of a] is the nucleotide base sequence of [selected from the group consisting of SEQ ID NO: 2,] SEQ ID NO: 22 or the sequence perfectly complementary thereto [, and their a fully complementary sequences of the same length].

68. (Twice Amended) The primer oligonucleotide of claim 67, [wherein the] said primer oligonucleotide [is] being from 15 to 50 [nucleotides] nucleotide bases in length.

69. (Twice Amended) The primer oligonucleotide of claim 67, said primer oligonucleotide comprising [a] the nucleotide base sequence [selected from the group consisting] of [SEQ ID NO: 2,] SEQ ID NO: 22[, and their fully complementary sequences of the same length] or the sequence perfectly complementary thereto.

70. (Three Times Amended) The primer oligonucleotide of claim 67, wherein the nucleotide base sequence of said primer oligonucleotide [consisting of] consists of or is contained within [a] the nucleotide base sequence [selected from the group consisting] of [SEQ ID NO: 2,] SEQ ID NO: 22[, and their fully complementary sequences of the same length] or the sequence perfectly complementary thereto.

71. (Twice Amended) The primer oligonucleotide of claim 67 [which] further [comprises, in the 5' upstream region,] comprising a nucleotide base sequence which is [recognizable] recognized by an RNA polymerase [and enhances initiation or elongation by said RNA polymerase] which initiates transcription.

72. (Three Times Amended) The primer oligonucleotide of claim 71, said primer oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 19.

73. (Three Times Amended) The oligonucleotide primer of claim 71, wherein the nucleotide base sequence of said primer oligonucleotide [consisting] consists of or is contained within a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 19.

75. (Three Times Amended) A composition for amplification of *Mycobacterium tuberculosis* nucleic acid, said composition comprising: [first and a second primer oligonucleotides, wherein said]

a first primer oligonucleotide consisting of an oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO:23 or the sequence perfectly complementary thereto [consists of the primer oligonucleotide of claim 147,]; and [said]

a second primer oligonucleotide [consists] consisting of an oligonucleotide of from about 10 to about 100 nucleotide bases in length which [will, under nucleic acid amplification conditions, hybridize] hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, [selected from the group consisting

of:] wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 7 or the sequence perfectly complementary thereto [and its complement].

76. CANCELED

77. CANCELED

78. (Three Times Amended) The composition of [any one of claims] claim 75[, 76, or 77], wherein at least one of said first and second [one or more] primer oligonucleotides further comprises[, in the 5' upstream region,] a nucleotide base sequence which is recognized by an RNA polymerase [and] which [enhances] initiates transcription [initiation or polymerization by said RNA polymerase].

79. (Four Times Amended) The composition of [any one of claims] claim 75[, 76, or 77,] further comprising a [nucleic acid] hybridization [assay] probe of from about 10 to about 100 nucleotide bases in length which [will hybridize with] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under [hybridization] reaction conditions, wherein the nucleotide base sequence of said region is [selected from the group consisting] the nucleotide base sequence of SEQ ID NO: 8 [and] or the sequence perfectly complementary [sequence] thereto.

80. (Twice Amended) The composition of claim 79, wherein said probe comprises [an oligonucleotide] a nucleotide base sequence selected from the group consisting of SEQ ID NO: 8 and the sequence perfectly complementary [sequence] thereto.

82. (Three Times Amended) The composition of claim 79, wherein said probe [contains] further comprises a detectable label.

83. (Amended) The composition of claim 82, wherein said detectable label is an acridinium ester.

84. (Three Times Amended) A composition [able] for amplification of *Mycobacterium tuberculosis* nucleic acid, said composition comprising[: one or more] first and second primer oligonucleotides, each of said primer oligonucleotides being from about 10 to about 100 nucleotide bases in length, [which]

wherein said first primer oligonucleotide [will, under nucleic acid amplification conditions, hybridize] hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said region [consisting of a] is the nucleotide base sequence[, said region selected from the group consisting] of[: a)] SEQ ID NO: 22[, b) SEQ ID NO: 2, and c) a nucleotide sequence or the sequence perfectly complementary], and

wherein said second primer oligonucleotide hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 2.

85. CANCELED

86. (Twice Amended) The composition of claim 84, wherein [comprising a] said first primer oligonucleotide [which] comprises [a] the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 22, and wherein said second primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 2.

87. CANCELED

88. (Twice Amended) The composition of [any one of claims] claim 84[, 85,] or 86, wherein at least one of said [one or more] first and second primer oligonucleotides further comprises[, in the 5' upstream region,] a nucleotide base sequence which is recognized by an RNA polymerase [and] which [enhances] initiates transcription [initiation or polymerization by said RNA polymerase].

89. (Twice Amended) The composition of [any one] of [claims] claim 84[,] or 86[, or 87,] further comprising a [nucleic acid] hybridization [assay] probe of from about 10 to about 100 nucleotide bases in length which [will hybridize with] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under [hybridization] reaction conditions, wherein the nucleotide base sequence of said region [consisting of] consists of the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary [sequence] thereto.

90. (Amended) The composition of claim 89, wherein said probe comprises [an oligonucleotide with a] the nucleotide base sequence [comprising] of SEQ ID NO: 3 or the sequence perfectly complementary [sequence] thereto.

91. CANCELED

92. (Amended) The composition of claim [84] 89, wherein said probe [contains] comprises a detectable label.

96. (Twice Amended) A probe mix comprising:

a [nucleic acid] hybridization [assay] probe [comprising an oligonucleotide] of from 10 to 100 nucleotides in length which [will hybridize with] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis*

nucleic acid to form a detectable hybridization duplex under [selective hybridization] reaction conditions, wherein the nucleotide base sequence of said region is [selected from the group consisting of] the nucleotide base sequence of SEQ ID [NO. 8] NO: 8 or the sequence perfectly complementary thereto [and its fully complementary sequence of the same length,]; and

a helper [probe] oligonucleotide.

97. (Amended) The probe mix of claim 96, wherein said helper [probe] oligonucleotide consists essentially of a nucleic acid sequence selected from the group consisting of[:] SEQ ID NO: 9[,] and SEQ ID NO: 10.

98. (Amended) A probe mix comprising:

a [nucleic acid] hybridization [assay] probe [comprising an oligonucleotide] of from 10 to 100 [nucleotides] nucleotide bases in length which [will hybridize with] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under [selective hybridization] reaction conditions, wherein the nucleotide base sequence of said region [consists] is the nucleotide base sequence of SEQ ID [NO. 3,] NO: 3 or the sequence perfectly complementary thereto [its fully complementary sequence of the same length,]; and

a helper [probe] oligonucleotide.

99. (Amended) The probe mix of claim 98, wherein said helper [probe] oligonucleotide consists essentially of a nucleic acid sequence selected from the group consisting of[:] SEQ ID NO: 4[,] and SEQ ID NO: 5.

100. (Three Times Amended) A kit for amplifying *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide comprising xCCAGGCCACTTCCGCTAACC ([SEQ ID: 6] SEQ ID NO: 23)[,]; and

a second oligonucleotide comprising xCGCGGAACAGGCTAAACCGCACGC ([SEQ ID: 7] SEQ ID NO: 7),

wherein x is nothing or is a sequence recognized by an RNA polymerase.

101. (Three Times Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising [at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of]:

a) a [nucleic acid] hybridization [assay] probe of from about 10 to about 100 nucleotide bases in length comprising [an oligonucleotide] a nucleotide base sequence which [will hybridize] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of a target] present in *Mycobacterium tuberculosis* nucleic acid, wherein the nucleotide base sequence of said region is a nucleotide sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 8 and the [nucleotide] sequences perfectly complementary thereto; and

b) [at least one] a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length [able to hybridize] which hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region [consisting of a] is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 22, SEQ ID NO: 23, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

102. (Amended) A composition comprising:

[a nucleic acid comprising a (+) target sequence,]

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3'[-] end of said (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first [oligonucleotide] primer sequence which reduces or blocks extension

of said first [oligonucleotide] primer sequence by a polymerase compared to said first [oligonucleotide] primer sequence not having said modification[,];

a second oligonucleotide comprising a second primer sequence able to hybridize at or near [said] the 3'[-] end of [said] a (+) target nucleic acid sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second [oligonucleotide] primer sequence which reduces or blocks extension of said second [oligonucleotide] primer sequence by a polymerase compared to said second [oligonucleotide] primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second [oligonucleotide modification] primer sequence, if present, is different than said modification to said first [oligonucleotide] primer sequence [modification,];

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3'[-] end of a (-) target nucleic acid sequence [which is produced during said method and] which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third [oligonucleotide] primer sequence [able to reduce or block] which reduces or blocks extension of said third [oligonucleotide] primer sequence by a polymerase compared to said third [oligonucleotide] primer sequence not having said modification[,];

an enzyme selected from the group consisting of a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase[,]; and

one or more RNA polymerases that recognize said promoter sequence of said first and [said] second [oligonucleotide 5' promoter sequences] oligonucleotides.

108. (Amended) The composition of claim 102[,] further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

109. (Amended) The composition of claim 102[,] further comprising a helper oligonucleotide.

111. (Amended) The composition of claim 102, wherein said second [oligonucleotide contains said] primer sequence comprises said modification at or near its 3' end.

112. (Amended) The composition of claim 111[,] further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said first and second oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth [oligonucteotide] primer sequence does not contain a modification at or near its 3' end [to reduce or block primer] which reduces or blocks extension of said fourth [oligonucleotide] primer sequence.

113. (Amended) The composition of claim [102] 111, wherein the 3' end modifications to said first [oligonucleotide modification and said second oligonucleotide modification] and second primer sequences are [each] independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

114. (Amended) The composition of claim [102] 111, wherein the 3' end modifications to said first [oligonucleotide modification and said second oligonucleotide modification] and second primer sequences are [each] independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

115. (Amended) The composition of claim 102, wherein said third [oligonucleotide] primer sequence does not [contain said] comprise said modification at or near its 3' end.

116. (Amended) The composition of claim 102, wherein said third oligonucleotide [contains] comprises said 5' promoter sequence.

117. (Amended) The composition of claim 116, wherein said third [oligonucleotide contains said] primer sequence comprises said modification at or near its 3' end.

118. (Amended) The composition of claim 102, wherein said first and [said] second [oligonucleotide] primer sequences are the same.

119. (Amended) The composition of claim 102, wherein said first and [said] second [oligonucleotide] primer sequences are different.

120. (Amended) A composition comprising:

[a nucleic acid comprising a (+) target sequence,]

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3'[-] end of [said] a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first [oligonucleotide] primer sequence [able to reduce or block] which reduces or blocks extension of said first [oligonucleotide] primer sequence by a polymerase compared to said first [oligonucleotide] primer sequence not having said modification[,];

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3'[-]end of a (-) target nucleic acid sequence [which is produced during said method and] which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at

or near the 3' end of said second [oligonucleotide] primer sequence which reduces or blocks extension of said second [oligonucleotide] primer sequence by a polymerase compared to said second [oligonucleotide] primer sequence not having said modification[,];

a third oligonucleotide comprising a third primer sequence able to hybridize at or near [said] the 3'[-] end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third [oligonucleotide] primer sequence which reduces or blocks extension of said third [oligonucleotide] primer sequence by a polymerase compared to said third [oligonucleotide] primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide, and wherein said modification to said third oligonucleotide [modification], if present, is different than said modification to said second oligonucleotide [modification,];

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase[,]; and

one or more RNA polymerases that recognize said promoter sequences of said first and [said] second [oligonucleotide 5' promoter sequences] oligonucleotides.

126. (Amended) The composition of claim 120[,] further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

127. (Amended) The composition of claim 120[,] further comprising a helper oligonucleotide.

129. (Amended) The composition of claim 120, wherein said third [oligonucleotide contains] primer sequence comprises said modification at its 3' end.

130. (Amended) The composition of claim 129[,] further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said second and third oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth [oligonucleotide] primer sequence does not [contain] comprise a modification at or near its 3' end [to reduce or block] which reduces or blocks primer extension of said fourth [oligonucteotide] primer sequence.

131. (Amended) The composition of claim [120] 129, wherein said 3' end modifications to said second [oligonucleotide modification and said third oligonucleotide modification] and third primer sequences are [each] independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

132. (Amended) The composition of claim [120] 129, wherein the 3' end modifications to said [first oligonucleotide modification and said second oligonucleotide modification] second and third primer sequences are [each] independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

133. (Amended) The composition of claim 120, wherein said first [oligonucleotide] primer sequence does not [contain said] comprise said modification at or near its 3' end.

134. (Amended) The composition of claim 120, wherein said first oligonucleotide [contains] comprises said 5' promoter sequence.

135. (Amended) The composition of claim 120, wherein said [third] first [oligonucleotide contains said] primer sequence comprises said modification at or near its 3' end.

136. (Amended) The composition of claim 134, wherein said promoter sequences of said first, second and third oligonucleotides [oligonucleotide 5'promoter sequence, said second oligonucleotide 5' promoter sequence and said third oligonucleotide 5' promoter sequence] are the same.

137. (Amended) The composition of claim 120, wherein said promoter sequences of said second and [said] third [oligonucleotide] primer sequences are the same.

138. (Amended) The composition of claim 120, wherein said promoter sequences of said second and said third [oligonucleotide] primer sequences are different.

139. (Amended) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3'[-] end of a (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first [oligonucleotide] primer sequence which reduces or blocks extension of said first [oligonucleotide] primer sequence by a polymerase compared to said first [oligonucleotide] primer sequence not having said modification[,];

a second oligonucleotide comprising a second primer sequence able to hybridize at or near [said] the 3'[-] end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second [oligonucleotide] primer sequence which reduces or blocks extension of said second [oligonucleotide] primer sequence by a polymerase compared to said second [oligonucleotide] primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second [oligonucleotide

modification] primer sequence, if present, is different than said modification to said first [oligonucleotide modification,] primer sequence;

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3'[-] end of a (-) target nucleic acid sequence [which is produced during said method and] which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third [oligonucleotide] primer sequence [able to reduce or block] which reduces or blocks extension of said third [oligonucleotide] primer sequence by a polymerase compared to said third [oligonucleotide] primer sequence not having said modification[,];

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase[,]; and

one or more RNA polymerases that recognize said promoter sequences of said first and [said] second [oligonucleotide 5' promoter sequences] oligonucleotides.

140. (Amended) The kit of claim 139[,] further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

141. (Amended) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3'[-] end of a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first [oligonucleotide] primer sequence [able to reduce or block] which reduces or blocks extension of said first [oligonucleotide] primer sequence by a polymerase compared to said first [oligonucleotide] primer sequence not having said modification[,];

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3'[-] end of a (-) target nucleic acid sequence [which is produced during said method and] which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at

or near the 3' end of said second [oligonucleotide] primer sequence which reduces or blocks extension of said second [oligonucleotide] primer sequence by a polymerase compared to said second [oligonucleotide] primer sequence not having said modification[,];

a third oligonucleotide comprising a third primer sequence able to hybridize at or near [said] the 3'[-] end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third [oligonucleotide] primer sequence which reduces or blocks extension of said third [oligonucleotide] primer sequence by a polymerase compared to said third [oligonucleotide] primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide and said modification to said third oligonucleotide [modification], if present, is different than said modification to said second oligonucleotide [modification,];

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase[,]; and

one or more RNA polymerases that recognize said promoter sequences of said first and [said] second [oligonucleotide 5' promoter sequences] oligonucleotides.

142. (Amended) The kit of claim 141[,] further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

143. (Twice Amended) An oligonucleotide of from [about] 20 to about 100 bases in length, said oligonucleotide comprising a nucleotide base sequence [consisting of a nucleic acid sequence] selected from the group consisting of xCCAGGCCACTTCCGCTAACC ([SEQ ID: 6 or 23] SEQ ID NO: 23), xCGCGGAACAGGCTAAACCGCACGC ([SEQ ID: 7] SEQ ID NO: 7), and [their fully complementary sequences of the same length] the sequences perfectly complementary thereto, wherein x is nothing or [is] a sequence recognized by an RNA polymerase.

144. (Twice Amended) [A] The composition [comprising two or more oligonucleotides] of claim 143, wherein [one or more of said oligonucleotides] said oligonucleotide [is modified at the] has a 3' end which is modified to reduce or block extension of said [one or more of said oligonucleotides] oligonucleotide by a polymerase.

145. (Twice Amended) A composition comprising: [two or more oligonucleotides of claim 143, wherein one or more of said oligonucleotides is unmodified at the 3' end and one or more of said oligonucleotides]

a first oligonucleotide in accordance with said oligonucleotide of claim 143, wherein said first oligonucleotide has a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide in accordance with said oligonucleotide of claim 143, wherein said second oligonucleotide has a 3' end which is modified [at the 3' end] to reduce or block extension of said second oligonucleotide by a polymerase.

146. (Twice Amended) The composition of claim 145 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension of said third oligonucleotide by a polymerase, wherein [one or more of] the 3' ends of said second and third oligonucleotides [is] are differently modified [at the 3' end to reduce or block extension by a polymerase].

147. (Twice Amended) A primer oligonucleotide of from 10 to 100 nucleotide bases in length [able to hybridize] which hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region [consists of a] is the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 23[, and the fully complementary sequence of the same length thereof] or the sequence perfectly complementary thereto.

148. (Amended) The primer oligonucleotide of claim 147, wherein [the] said primer oligonucleotide is from 15 to 50 [nucleotides] nucleotide bases in length.

149. (Amended) The primer oligonucleotide of claim 147, wherein [the] said primer oligonucleotide is from about 20 to about 100 [nucleotides] nucleotide bases in length.

150. (Amended) The primer oligonucleotide of claim 69, wherein [the] said primer oligonucleotide is from [about 20] 22 to about 100 [nucleotides] nucleotide bases in length.

151. (Twice Amended) The primer oligonucleotide of claim 147, [comprising] wherein said primer oligonucleotide comprises [a] the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 23[, and the fully complementary sequence of the same length thereof] or the sequence perfectly complementary thereto.

152. (Twice Amended) The primer [oligonucleotide] of claim 147, [consisting of or contained] wherein the nucleotide base sequence of said primer consists of or is contained within [a] the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 23[, and the fully complementary sequence of the same length thereof] or the sequence perfectly complementary thereto.

153. (Amended) The primer [oligonucleotide] of claim 147 [which further comprises, in the 5' upstream region,] further comprising a nucleotide base sequence which is [recognizable] recognized by an RNA polymerase [and enhances initiation or elongation by said RNA polymerase] which initiates transcription.

154. (Amended) The primer [oligonucleotide] of claim 153, [comprising] wherein said primer comprises [a] the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 6 [and] or SEQ ID NO: 19.

155. (Amended) The primer [oligonucleotide] of claim 153, [consisting of or contained] wherein the nucleotide base sequence of said primer consists of or is contained within [a] the nucleotide base sequence [selected from the group consisting] of SEQ ID NO: 6 [and] or SEQ ID NO: 19.

156. (Amended) The composition of claim 82 further comprising:

a first [and second] helper [oligonucleotides] oligonucleotide[, wherein the first helper oligonucleotide comprises] comprising the nucleotide base sequence of SEQ ID NO:9; and

[the] a second helper oligonucleotide [comprises] comprising the nucleotide base sequence of SEQ ID NO: 10.

157. (Amended) The composition [according to] of claim 101 further comprising [at least one] a helper [probe] oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9, SEQ ID NO: 10, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

158. (Amended) A kit comprising a primer oligonucleotide of [claim 101] from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 22, SEQ ID NO: 23, and the sequences perfectly complementary thereto.

159. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under [nucleic acid hybridization] reaction conditions between [the nucleic acid hybridization assay probe of claim 101 and a nucleic acid comprising] a nucleotide base sequence region present in *Mycobacterium tuberculosis* [nucleotide base sequence] nucleic acid, or a sequence perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 8, and the RNA equivalents.

160. (Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising [at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of]:

a) a [nucleic acid] hybridization [assay] probe of from about 10 to about 100 nucleotide bases in length comprising [an oligonucleotide] a nucleotide base sequence which [will hybridize] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region [of a target] present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region [selected from the group consisting] is the nucleotide base sequence of SEQ ID NO: 3 [and the nucleotide sequences] or the sequence perfectly complementary thereto; and

b) [at least one] a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length [able to hybridize] which hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is [consisting of a nucleotide base sequence] selected from the group consisting of [SEQ ID NO: 1,] SEQ ID NO: 22, SEQ ID NO: 2, and [the nucleotide] sequences perfectly complementary [to these sequences] thereto.

161. (Amended) The composition [according to] of claim 160 further comprising [at least one] a helper [probe] oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

162. (Amended) A kit comprising a primer oligonucleotide of [claim 160] from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto.

163. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under [nucleic acid hybridization] reaction conditions between [the nucleic acid hybridization assay probe of claim 160 and a nucleic acid comprising] a nucleotide base sequence region present in *Mycobacterium tuberculosis* [nucleotide base sequence] nucleic acid, or a sequence perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 3 or the RNA equivalent thereof.

164. (Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising [at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of]:

a) a [nucleic acid] hybridization [assay] probe of from about 10 to about 100 nucleotide bases in length comprising [an oligonucleotide] a nucleotide base sequence which [will hybridize] hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence

region [of a target] present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of [selected from the group consisting] SEQ ID NO: 8 [and the nucleotide sequences] or the sequence perfectly complementary thereto; and

b) [at least one] a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length [able to hybridize] which hybridizes to a nucleotide base sequence region [of] present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region [consisting of a] is a nucleotide base sequence selected from the group consisting of [SEQ ID NO: 6,] SEQ ID NO: 23, SEQ ID NO: 7, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

165. (Amended) The composition [according to] of claim 164 further comprising [at least one] a helper [probe] oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

166. (Amended) A kit comprising a primer oligonucleotide of [claim 164] from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 7, and the sequences perfectly complementary thereto.

167. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under [nucleic acid hybridization] reaction conditions between [the nucleic acid hybridization assay probe of claim 164 and a nucleic acid comprising a] a nucleotide base sequence region present in *Mycobacterium tuberculosis* [nucleotide base sequence] nucleic acid, or a sequence

perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8.

168. (Amended) The kit [according to] of claim 41 further comprising [at least one] a helper [probe] oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

169. (Amended) The kit [according to] of claim 42 further comprising [at least one] a helper [probe] oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, and the [nucleotide] sequences perfectly complementary [to these sequences] thereto.

170. (Amended) The composition of claim 80, wherein said probe [contains] further comprises a detectable label.

171. (Amended) The composition of claim 170, wherein said detectable label is an acridinium ester.

172. (Amended) The composition of claim 170 further comprising:

a first [and second] helper [oligonucleotides] oligonucleotide[, wherein the first helper oligonucleotide comprises] comprising the nucleotide base sequence of SEQ ID NO: 9; and

[the] a second helper oligonucleotide [comprises] comprising the nucleotide base sequence of SEQ ID NO: 10.